

CRF Errors Corrected by the STIC Systems Branch

0300

OIPE

Serial Number: 09/885,297A

CRF Processing Date: 3/27/02

Edited by:

Verified by: DC (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: **ENTERED**
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☒ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/885,297A

DATE: 03/27/2002 P.6

TIME: 16:35:19

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\03272002\I885297A.raw

3 <110> APPLICANT: Ingram, Lonnie O
 4 Zhou, Shengde
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SIMULTANEOUS
 7 SACCHARIFICATION AND FERMENTATION
 9 <130> FILE REFERENCE: BCI-024CP
 11 <140> CURRENT APPLICATION NUMBER: 09/885,297A
 C--> 12 <141> CURRENT FILING DATE: 2001-06-19
 14 <150> PRIOR APPLICATION NUMBER: 60/214,137
 15 <151> PRIOR FILING DATE: 2000-06-26
 17 <150> PRIOR APPLICATION NUMBER: 60/219,913
 18 <151> PRIOR FILING DATE: 2000-07-21
 20 <160> NUMBER OF SEQ ID NOS: 17
 22 <170> SOFTWARE: PatentIn Ver. 2.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 450
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Zymomonas mobilis
 29 <400> SEQUENCE: 1
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 32 cggtttagcca taaccatttt acctgtccgg cggccttaac acctgatca gatggttcgt 120
 34 ggtggttgta ccttgccgaa gggcaccggt aaaaatgttc gcgtcgggtgt tttcgcccg 180
 36 ggcccgaaag ctgaagaagc taaagctgct ggtgcagaag ttgtcggcgc agaagacctg 240
 38 atggaagcca ttcagggcgg cagcattgat ttcgatcgtg atgcccttta tactgaaatt 300
 40 gccttgcgct gccataatga agcagcctcc ggtgttttgg cagatttaag cgctgcctga 360
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 44 ataaccatcc agtcatccgc aagcttggcc 450
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 48 <211> LENGTH: 1509
 49 <212> TYPE: DNA
 50 <213> ORGANISM: Zymomonas mobilis
 52 <400> SEQUENCE: 2
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 57 gcatggacat cccagacatt gggattgaac ctgtttggtg tcatgctttt gattacgact 180
 59 tttgctaccc tgatttcgga tattaccggt tttcagtcatt ggcaaaccct gctgcattac 240
 61 ggtttcaaaag cttttcagga aaaagatttt aaccaatttg atgatgtcct tgccttttgc 300
 63 atcagagccg atttttttag tgcggcgata ggtatgttgg tagggttagg cggatatctg 360
 65 atttttaggca cttcaagatt gggatggcct gccagagtca agccagatgc cttgctttgt 420
 67 atgctgatta tactttttat gaatatcggc tgggtccaacc gggatgttgc ggctgtgtaa 480
 69 ccgcttttaa ctgggtcacta tttatgagtt tattacgacc tgcgtcagaa ccggagggtg 540
 71 tggcattggt tattggcttc atatgccttt ggggtatttt ttgtttatat ggtgcctgac 600
 73 gcaattcaag ctttttgtca cctgtagtta cgctggcatt tatctctttc accaatatac 660
 75 ggagcgagca tttccgataa gaaaaatatt tcagagaaaa acgcccgttg aagggatgtg 720

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79 cacccttgct attggtagct cactgggggc tggggaagcc gctgtctatc gggtcgcgcg 840
81 ccagattagt aacggtttat ccaaaccagc acagatgatg atcggctaac atgcatccac 900
83 cggcagcacc ggccgtttta tgcttgggat tattgatatg ccgaaaagga tacaacatct 960
85 ggaagaaaaa gacgaaggcc ggaataagcg cccattctgc aaaattgtta caacttagtc 1020
87 gcgccatcag ggaatgaaaa atcaatccgt ctttttcggc atgagcaacc aacattttca 1080
89 aggtatcatc ctgatgcgca atatcggcac cggttagcca taaccatttt acctgtccgg 1140
91 cggccttaat acctgatca gatggttcgt ggtgttgta ccttgccgaa gggcacccgg 1200
93 aaaaatgttc gcgtcgggtg tttcgcccg ggcccgaaag ctgaagaagc taaagtgtct 1260
95 ggtgcagaag ttgtcggcgc agaagacctg atggaagcca ttcagggcgg cagcattgat 1320
97 ttcgatcgtg atgcccttta tactgaaatt gccttgcgct gccataatga agcagcctcc 1380
99 ggtgttttgg cagatttaag cgctgcctga ttttcgtgat cctctagagt ctatgaaatg 1440
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103 gtaatccat 1509
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119 <211> LENGTH: 31
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121 <213> ORGANISM: Artificial Sequence
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
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136 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
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147 <220> FEATURE:
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154 <210> SEQ ID NO: 7
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RAW SEQUENCE LISTING

DATE: 03/27/2002

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Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\03272002\I885297A.raw

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203 <211> LENGTH: 8
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215 <211> LENGTH: 11544
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: Description of Artificial Sequence:vector
222 <220> FEATURE:
223 <221> NAME/KEY: misc_feature
224 <222> LOCATION: 3282-4281
225 <223> OTHER INFORMATION: n=a,c,g or t
227 <220> FEATURE:
228 <221> NAME/KEY: misc_feature

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RAW SEQUENCE LISTING

DATE: 03/27/2002

PATENT APPLICATION: US/09/885,297A

TIME: 16:35:19

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Output Set: N:\CRF3\03272002\I885297A.raw

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 230 <223> OTHER INFORMATION: n=a,c,g or t
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 233 <223> OTHER INFORMATION: nucleotide positions 1-1451 encodes promoter
 235 <220> FEATURE:
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 238 <220> FEATURE:
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 242 <223> OTHER INFORMATION: nucleotide positions 7061-8251 encodes tet gene
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 245 <223> OTHER INFORMATION: nucleotide positions 9476-11544 encodes target sequence from
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 247 <220> FEATURE:
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 249 <222> LOCATION: (1452)..(2735)
 251 <220> FEATURE:
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 255 <220> FEATURE:
 256 <221> NAME/KEY: CDS
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 264 gcatggacat ccagacatt gggattgaac ctgtttgggt tcatgctttt gattacgact 180
 266 tttgctaccc tgatttcgga tattaccctg tttcagtcac ggcaaaccct gctgcattac 240
 268 ggttcaaaag cttttcagga aaaagatttt aaccaatttg atgatgtcct tgccttttgc 300
 270 atcagagccg atttttttag tgcggcgata ggtatgttgg taggggttag cggatatctg 360
 272 attttaggca cttcaagatt gggatggcct gccgaggtca agccagatgc cttgctttgt 420
 274 atgctgatta tactttttat gaatatcggc tggccaacc gggatgttgc ggctgtgtaa 480
 276 ccgctttaaa ctggtcacta tttatgagtt tattacgacc tgcgtcagaa ccggaggttg 540
 278 tggcattggt tattggcttc atatgccttt ggggtatttt ttgtttatat ggtgcctgac 600
 280 gcaattcaag ctttttgtca cctgtagtta cgctggcatt tatctctttc accaatatac 660
 282 ggagcgagca tttccgataa gaaaaatatt tcagagaaaa acgcccgttg aagggatgtg 720
 284 gaaattcact ttaagcgtca gttttaatga aatcctagac tccattttcc agcaggttg 780
 286 cacccttgct attggtagct cactgggggc tggggaagcc gctgtctatc gggtcgcgcg 840
 288 ccagattagt aacggtttat ccaaaccagc acagatgatg atcggctaac atgcatccac 900
 290 cggcagcacc ggccgtttta tgcttgggat tattgatatg ccgaaaagga tacaacatct 960
 292 ggaagaaaaa gacgaaggcc ggaataagcg ccattctgct aaaattgtta caacttagtc 1020
 294 gcgcatcag ggaatgaaaa atcaatccgt ctttttcggc atgagcaacc aacattttca 1080
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 300 aaaaatgttc gcgtcgggtgt tttcgcccggt ggcccgaaag ctgaagaagc taaagctgct 1260
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 306 ggtgttttgg cagatttaag cgctgcctga ttttcgtgat cctctagagt ctatgaaatg 1440
 308 gagattcatt t atg cct ctc tct tat tcg gat aac cat cca gtc atc gat 1490
 309 Met Pro Leu Ser Tyr Ser Asp Asn His Pro Val Ile Asp
 310 1 5 10

RAW SEQUENCE LISTING

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TIME: 16:35:19

Input Set : A:\PTO.DC.txt

Output Set: N:\CRF3\03272002\I885297A.raw

312	agc	caa	aaa	cac	gcc	cca	cgt	aaa	aaa	ctg	ttt	cta	tct	tgt	gcc	tgt	1538
313	Ser	Gln	Lys	His	Ala	Pro	Arg	Lys	Lys	Leu	Phe	Leu	Ser	Cys	Ala	Cys	
314		15					20				25						
316	tta	gga	tta	agc	ctt	gcc	tgc	ctt	tcc	agt	aat	gcc	tgg	gcg	agt	gtt	1586
317	Leu	Gly	Leu	Ser	Leu	Ala	Cys	Leu	Ser	Ser	Asn	Ala	Trp	Ala	Ser	Val	
318	30					35				40						45	
320	gag	ccg	tta	tcc	gtt	agc	ggc	aat	aaa	atc	tac	gca	ggg	gaa	aaa	gcc	1634
321	Glu	Pro	Leu	Ser	Val	Ser	Gly	Asn	Lys	Ile	Tyr	Ala	Gly	Glu	Lys	Ala	
322					50					55					60		
324	aaa	agt	ttt	gcc	ggc	aac	agc	tta	ttc	tgg	agt	aat	aat	ggg	tgg	ggg	1682
325	Lys	Ser	Phe	Ala	Gly	Asn	Ser	Leu	Phe	Trp	Ser	Asn	Asn	Gly	Trp	Gly	
326				65				70						75			
328	ggg	gaa	aaa	ttc	tac	aca	gcc	gat	acc	gtt	gcg	tcg	ctg	aaa	aaa	gac	1730
329	Gly	Glu	Lys	Phe	Tyr	Thr	Ala	Asp	Thr	Val	Ala	Ser	Leu	Lys	Lys	Asp	
330			80					85					90				
332	tgg	aaa	tcc	agc	att	gtt	cgc	gcc	gct	atg	ggc	gtt	cag	gaa	agc	ggg	1778
333	Trp	Lys	Ser	Ser	Ile	Val	Arg	Ala	Ala	Met	Gly	Val	Gln	Glu	Ser	Gly	
334		95				100						105					
336	ggg	tat	ctg	cag	gac	ccg	gct	ggc	aac	aag	gcc	aaa	gtt	gaa	aga	gtg	1826
337	Gly	Tyr	Leu	Gln	Asp	Pro	Ala	Gly	Asn	Lys	Ala	Lys	Val	Glu	Arg	Val	
338	110					115					120					125	
340	gtg	gat	gcc	gca	atc	gcc	aac	gat	atg	tat	gtg	att	att	gac	tgg	cac	1874
341	Val	Asp	Ala	Ala	Ile	Ala	Asn	Asp	Met	Tyr	Val	Ile	Ile	Asp	Trp	His	
342					130					135					140		
344	tca	cat	tct	gca	gaa	aac	aat	cgc	agt	gaa	gcc	att	cgc	ttc	ttc	cag	1922
345	Ser	His	Ser	Ala	Glu	Asn	Asn	Arg	Ser	Glu	Ala	Ile	Arg	Phe	Phe	Gln	
346				145				150						155			
348	gaa	atg	gcg	cgc	aaa	tat	ggc	aac	aag	ccg	aat	gtc	att	tat	gaa	atc	1970
349	Glu	Met	Ala	Arg	Lys	Tyr	Gly	Asn	Lys	Pro	Asn	Val	Ile	Tyr	Glu	Ile	
350			160					165						170			
352	tac	aac	gag	ccg	ctt	cag	gtt	tca	tgg	agc	aat	acc	att	aaa	cct	tat	2018
353	Tyr	Asn	Glu	Pro	Leu	Gln	Val	Ser	Trp	Ser	Asn	Thr	Ile	Lys	Pro	Tyr	
354		175				180						185					
356	gcc	gaa	gcc	gtg	att	tcc	gcc	att	cgc	gcc	att	gac	ccg	gat	aac	ctg	2066
357	Ala	Glu	Ala	Val	Ile	Ser	Ala	Ile	Arg	Ala	Ile	Asp	Pro	Asp	Asn	Leu	
358	190					195					200				205		
360	att	att	gtc	ggg	acg	ccc	agt	tgg	tcg	caa	aac	gtt	gat	gaa	gcg	tcg	2114
361	Ile	Ile	Val	Gly	Thr	Pro	Ser	Trp	Ser	Gln	Asn	Val	Asp	Glu	Ala	Ser	
362				210						215					220		
364	cgc	gat	cca	atc	aac	gcc	aag	aat	atc	gcc	tat	acg	ctg	cat	ttc	tac	2162
365	Arg	Asp	Pro	Ile	Asn	Ala	Lys	Asn	Ile	Ala	Tyr	Thr	Leu	His	Phe	Tyr	
366				225				230						235			
368	gcg	gga	acc	cat	ggg	gag	tca	tta	cgc	act	aaa	gcc	cgc	cag	gcg	tta	2210
369	Ala	Gly	Thr	His	Gly	Glu	Ser	Leu	Arg	Thr	Lys	Ala	Arg	Gln	Ala	Leu	
370			240					245						250			
372	aat	aac	ggg	att	gcg	ctt	ttc	gtc	acc	gag	tgg	ggc	gcc	gtt	aac	gcg	2258
373	Asn	Asn	Gly	Ile	Ala	Leu	Phe	Val	Thr	Glu	Trp	Gly	Ala	Val	Asn	Ala	
374			255					260						265			
376	gac	ggc	aat	ggc	gga	gtg	aac	cag	aca	gat	acc	gac	gcc	tgg	gta	acg	2306

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/885,297A

DATE: 03/27/2002
TIME: 16:35:20

Input Set : A:\PTO.DC.txt
Output Set: N:\CRF3\03272002\I885297A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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 4 Zhou, Shengde
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 875 <222> LOCATION: 5753-7567
 876 <223> OTHER INFORMATION: n=a,c,g or t
 878 <220> FEATURE:
 879 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 880 construct
 882 <220> FEATURE:
 883 <223> OTHER INFORMATION: unsequenced Erwinia DNA fragment from nucleotide
 884 position 144 to 1143
 886 <220> FEATURE:
 887 <223> OTHER INFORMATION: P1 promoter region for celZ from nucleotide
 888 position 2974 to 4424
 890 <220> FEATURE:
 891 <223> OTHER INFORMATION: guide fragment for integration from nucleotide
 892 position 4677 to 7573
 894 <220> FEATURE:
 895 <223> OTHER INFORMATION: sequenced partial guide fragment from nucleotide

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902 <220> FEATURE:
903 <223> OTHER INFORMATION: P2 promoter region for cely from nucleotide
904      position 7585 to 8576
906 <220> FEATURE:
907 <223> OTHER INFORMATION: R6K-Y ori from nucleotide position 10388 to 10763
909 <220> FEATURE:
910 <223> OTHER INFORMATION: FRTF lipase-binding sequence from nucleotide
911      position 16 to 50
913 <220> FEATURE:
914 <223> OTHER INFORMATION: FRTFlipase-binding sequence from nucleotide
915      position 10058 to 10092
917 <220> FEATURE:
918 <223> OTHER INFORMATION: celZ gene product is encoded by the complement of
919      nucleotides 1690 to 2973
921 <220> FEATURE:
922 <223> OTHER INFORMATION: cely gene product is encoded by the nucleotides
923      8576 to 9574
925 <220> FEATURE:
926 <223> OTHER INFORMATION: kanamycin-resistance gene product is encoded by
927      the complement of nucleotides 10827 to 11621
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TIME: 10:39:43

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1109 cgtactatca acaggttgaa ctgcggatct tgcggccgca aaaattaaaa atgaagtttt 10800
1110 gacgggtatcg aacccagag tcccgctcag aagaactcgt caagaaggcg atagaaggcg 10860
1111 atgcgctgcg aatcgggagc ggcgataccg taaagcacga ggaagcggc agccattcg 10920
1112 ccgccaagct cttcagcaat atcacgggta gccaacgcta tgctctgata gcggtccgccc 10980
1113 acaccagcc gccacagtc gatgaatcca gaaaagcggc cattttccac catgatattc 11040
1114 ggcaagcagg catcgccat ggtcacgacg agatcctcgc cgtcgggcat ccgcgccttg 11100
1115 agcctggcga acagttcggc tggcgcgagc ccctgatgct cttcgtccag atcatcctga 11160
1116 tcgacaagac cggcttccat ccgagtacgt gctcgtcga tgcgatgttt cgcttgggtg 11220
1117 tcgaatgggc aggtagccg atcaagcgt tgcagccgcc gcattgcac agccatgatg 11280
1118 gatactttct cggcaggagc aaggtgagat gacaggagat cctgccccgg cacttcgccc 11340
1119 aatagcagcc agtcccttcc cgcttcagt acaacgtcga gcacagctgc gcaaggaacg 11400
1120 cccgtcgtgg ccagccacga tagccgcgct gcctcgtctt ggagttcatt cagggcaccg 11460
1121 gacaggtcgg tcttgacaaa aagaaccggg cgccctgcg ctgacagccg gaacacggcg 11520
1122 gcatcagagc agccgattgt ctgttggtgc cagtcatagc cgaatagcct ctccacccaa 11580
1123 gcggccggag aacctgcgtg caatccatct tgttcaatca tgcgaaacga tccctcatcct 11640
1124 gtctcttgat ccactagatt attgaagcat ttatcagggt tattgtctca tgagcggata 11700
1125 catatttgaa tgtatttaga aaaataaaca aataggggtt ccgcgcacat ttccccgaaa 11760
1126 agtgccacct gc 11772

```

E--> 1128 atty. docket no. bcI-024cP

6

- delete

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/885,297A

DATE: 03/25/2002

TIME: 10:39:44

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\03252002\I885297A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:436 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:438 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:440 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:448 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:450 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:454 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:456 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:460 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:462 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:464 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:466 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12

L:490 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:494 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:498 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:502 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:506 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:510 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:514 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:518 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:522 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:526 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:530 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:534 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:538 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:542 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:546 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:550 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:554 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:558 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:562 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:607 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:609 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:613 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:617 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:621 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:625 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:629 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:633 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:637 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:641 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

L:645 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12

VERIFICATION SUMMARY

DATE: 03/25/2002

PATENT APPLICATION: US/09/885,297A

TIME: 10:39:44

Input Set : A:\seqlist.txt

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L:649 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:653 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:657 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:661 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:665 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:669 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:673 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:677 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:681 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:689 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:693 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:697 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:701 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:705 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:12
L:747 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:749 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:753 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:755 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:757 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:759 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:765 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:769 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:779 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:781 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:783 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:785 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:787 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:791 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:799 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:803 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:807 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:809 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:811 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1128 M:254 E: No. of Bases conflict, LENGTH:Input:6 Counted:11792 SEQ:17

VERIFICATION SUMMARY

DATE: 03/25/2002

PATENT APPLICATION: US/09/885,297A

TIME: 10:39:44

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\03252002\I885297A.raw

L:1128 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:11

L:1128 M:112 C: (48) String data converted to lower case,

L:1128 M:252 E: No. of Seq. differs, <211>LENGTH:Input:11772 Found:11792 SEQ:17